

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME : Genset SA
(B) STREET : 24, RUE ROYALE
(C) CITY : PARIS
(E) COUNTRY : France
(F) POSTAL CODE (ZIP) : 75008

(ii) TITLE OF INVENTION: Lipoprotein-regulating medicaments

(iii) NUMBER OF SEQUENCES: 14

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy Disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: Win95
(D) SOFTWARE: Word

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

PheX(5) [AsnAsp]X(4) [PheTyrTrpLeu]X(6) PheX(5) GlyXTyrXPhe X[PheTyr] 31

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

[SerThr]XPhe [SerTh] Gly[PheTyr]Leu[LeuVal] [PheTyr]

9

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Leu Arg Cys Val Pro Arg Val Leu Gly Ser Ser Val Ala Gly Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Cys Tyr Ile Thr Phe Leu Glu Asp Leu Lys Ser Phe Val Lys Ser Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: Identical to 58 .. 73 in ref genbank :U49915
(B) LOCATION: 12..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTACATGGAT CCAGTCATGC CGAAGAT

27

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

- (ix) FEATURE:
(A) NAME/KEY: Identical to 745 .. 762 in ref genbank :U49915
(B) LOCATION: complement 11..28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CGACAACTCG AGTCAGTTGG TATCATGG

28

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

- (ix) FEATURE:
(A) NAME/KEY: fragment 117-245 of ref swissprot :P02745

(ix) FEATURE: (A) NAME/KEY: Consensus box corresponding to
SEQ ID 1 (B) LOCATION: 17-47

- (ix) FEATURE:
(A) NAME/KEY: Consensus box corresponding to SEQ ID 2
(B) LOCATION: 118-126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Phe Ser Ala Ile Arg Arg Asn Pro Pro Met Gly Gly Asn Val Val Ile
 1 5 10 15
 Phe Asp Thr Val Ile Thr Asn Gln Glu Glu Pro Tyr Gln Asn His Ser
 20 25 30
 Gly Arg Phe Val Cys Thr Val Pro Gly Tyr Tyr Tyr Phe Thr Phe Gln
 35 40 45
 Val Leu Ser Gln Trp Glu Ile Cys Leu Ser Ile Val Ser Ser Ser Arg
 50 55 60
 Gly Gln Val Arg Arg Ser Leu Gly Phe Cys Asp Thr Thr Asn Lys Gly
 65 70 75 80
 Leu Phe Gln Val Val Ser Gly Gly Met Val Leu Gln Leu Gln Gly
 85 90 95
 Asp Gln Val Trp Val Glu Lys Asp Pro Lys Lys Gly His Ile Tyr Gln
 100 105 110
 Gly Ser Glu Ala Asp Ser Val Phe Ser Gly Phe Leu Ile Phe Pro Ser
 115 120 125
 Ala

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: fragment 122-251 of ref swissprot :P02745

(ix) FEATURE:

- (A) NAME/KEY: Consensus box corresponding to SEQ ID 1
- (B) LOCATION: 19-49

(ix) FEATURE:

- (A) NAME/KEY: Consensus box corresponding to SEQ ID 2
- (B) LOCATION: 117-125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Phe Ser Ala Thr Arg Thr Ile Asn Val Pro Leu Arg Arg Asp Gln Thr
 1 5 10 15

[illegible]

(2) INFORMATION FOR SEQ ID NO: 9:

(ii) MOLECULE TYPE: PEPTIDE

(ix) FEATURE:

(ix) FEATURE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

10072159.020502
205020.6512/001

Ser Thr Gly Lys Phe Thr Cys Lys Val Pro Gly Leu Tyr Tyr Phe Val
35 40 45
Tyr His Ala Ser His Thr Ala Asn Leu Cys Val Leu Leu Tyr Arg Ser
50 55 60
Gly Val Lys Val Val Thr Phe Cys Gly His Thr Ser Lys Thr Asn Gln
65 70 75 80
Val Asn Ser Gly Gly Val Leu Leu Arg Leu Gln Val Gly Glu Gly Val
85 90 95
Trp Leu Ala Val Asn Asp Tyr Tyr Asp Met Val Gly Ile Gln Gly Ser
100 105 110
Asp Ser Val Phe Ser Gly Phe Leu Leu Phe Pro Asp
115 120

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 amino acids
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:
 (A) NAME/KEY: fragment 64-193 of translation from ref genbank

:M58583

- (ix) FEATURE:
 (A) NAME/KEY: Consensus box corresponding to SEQ ID 1
 (B) LOCATION: 23-53
 (ix) FEATURE:
 (A) NAME/KEY: Consensus box corresponding to SEQ ID 2
 (B) LOCATION: 120-128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Ser Ala Ile Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn
1 5 10 15
Arg Thr Met Ile Ile Tyr Phe Asp Gln Val Leu Val Asn Ile Gly Asn
20 25 30
Asn Phe Asp Ser Glu Arg Ser Thr Phe Ile Ala Pro Arg Lys Gly Ile
35 40 45
Tyr Ser Phe Asn Phe His Val Val Lys Val Tyr Asn Arg Gln Thr Ile
50 55 60

Gln Val Ser Leu Met Leu Asn Gly Trp Pro Val Ile Ser Ala Phe Ala
65 70 75 80

Gly Asp Gln Asp Val Thr Arg Glu Ala Ala Ser Asn Gly Val Leu Ile
85 90 95

Gln Met Glu Lys Gly Asp Arg Ala Tyr Leu Lys Leu Glu Arg Gly Asn
100 105 110

Leu Met Gly Gly Trp Lys Tyr Ser Thr Phe Ser Gly Phe Leu Val Phe
115 120 125

Pro Leu
130

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: fragment 115-244 of translation from ref genbank
:D45371

- (ix) FEATURE:
(A) NAME/KEY: Consensus box corresponding to SEQ ID 1
(B) LOCATION: 18-48

- (ix) FEATURE:
(A) NAME/KEY: Consensus box corresponding to SEQ ID 2
(B) LOCATION: 118-126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met Pro Ile
1 5 10 15

Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp Gly Ser
20 25 30

Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe Ala Tyr
35 40 45

His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe Lys Lys
50 55 60

Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn Asn Val

Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly Asp Gln
85 90
Val Trp Leu Gln Val Tyr Gly Asp Gly Asp His Asn Gly Leu Tyr Ala
100 105 110
Asp Asn Val Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Phe His Asp
115 120 125
Thr Asn
130

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mus musculus*

(ix) FEATURE:
(A) NAME/KEY: fragment 118-267 of translation from ref genbank
:U37222

(ix) FEATURE:
(A) NAME/KEY: Consensus box corresponding to SEQ ID 1
(B) LOCATION: 18-48

(ix) FEATURE:
(A) NAME/KEY: Consensus box corresponding to SEQ ID 2
(B) LOCATION: 118-126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Phe Ser Val Gly Leu Glu Thr Arg Val Thr Val Pro Asn Val Pro Ile
1 5 10 15
Arg Phe Thr Lys Ile Phe Tyr Asn Gln Asn His Tyr Asp Gly Ser
20 25 30
Thr Gly Lys Phe Tyr Cys Asn Ile Pro Gly Leu Tyr Tyr Phe Ser Tyr
35 40 45
His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe Lys Lys
50 55 60
Asp Lys Ala Val Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Lys Asn Val
65 70 75 80
Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly Asp Gln
85 90 95

Val Trp Leu Gln Val Tyr Gly Asp Gly Asp His Asn Gly Leu Tyr Ala
 100 105 110
 Asp Asn Val Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr His Asp
 115 120 125
 Thr Asn
 130

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PEPTIDE
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: fragment 1161-1286 of translation from ref
 genbank :U27109
- (ix) FEATURE:
 - (A) NAME/KEY: Consensus box corresponding to SEQ ID 1
 - (B) LOCATION: 17-47
- (ix) FEATURE:
 - (A) NAME/KEY: Consensus box corresponding to SEQ ID 2
 - (B) LOCATION: 116-124
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Phe Phe Ala Ser His Thr Tyr Gly Met Thr Ile Pro Gly Pro Ile Leu
 1 5 10 15
 Phe Asn Asn Leu Asp Val Asn Tyr Gly Ala Ser Tyr Thr Pro Arg Thr
 20 25 30
 Gly Lys Phe Arg Ile Pro Tyr Leu Gly Val Tyr Val Phe Lys Tyr Thr
 35 40 45
 Ile Glu Ser Phe Ser Ala His Ile Ser Gly Phe Leu Val Val Asp Gly
 50 55 60
 Ile Asp Lys Leu Ala Phe Glu Ser Glu Asn Ile Asn Ser Glu Ile His
 65 70 75 80
 Cys Asp Arg Val Leu Thr Gly Asp Ala Leu Leu Glu Leu Asn Tyr Gly
 85 90 95
 Gln Glu Val Trp Leu Arg Leu Ala Lys Gly Thr Ile Pro Ala Lys Phe

